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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

April 4, 2005, 14:47:11; Search time 0.001 Seconds (without alignments) 183.834 Million cell updates/sec Run on:

us-10-088-666-21 21

Title: Perfect score: Sequence:

1 ccaagtcaacaacgtagttgt 21

IDENTITY NUC Gapox 10.5 Scoring table:

356 seqs, 4377 residues Searched:

Total number of hits satisfying chosen parameters:

712

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 371 summaries

21pubdb:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 12.4 59.0 14 1 US-09-947-209A-20 Sequen 2 12.4 59.0 14 1 US-09-947-209A-20 Sequen 3 12.4 59.0 14 1 US-00-095-379-20 Sequen 6 12.4 59.0 14 1 US-10-099-379-20 Sequen 7 11.4 54.3 13 US-10-402-100-20 Sequen 1 US-10-402-100-20 Sequen 1 US-10-257-017B-70446 Sequen 1 US-10-257-017B-7046 Sequen 1 US-10-257-017B-70406 Sequen 1 US-10-257-017B-706032 Sequen 1 US-10-267-017B-706032 Sequen 1 US-10-267-017B-7099 Sequen 1 US-10-267-017B-7099 Sequen 1 US-10-267-017B-7099 Sequen 1 US-10-267-017B-7099 Sequen 1 US-10-257-017B-7099 Sequen 1 US-10-257-017B-7099 Sequen 1 US-10-257-017B-7099 Sequen 1 US-10-257-017B-7099 Sequen 2 US-10-257-017B-7099 Sequ	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓		Score	Match		8	aı	Description
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9 11.4 54.3 13 1 US-10-257-017B-216031 Sequen 11.4 54.3 13 1 US-10-257-017B-216031 Sequen 11.2 53.3 16 1 US-10-043-875-402 Sequen 12 10.6 50.5 15 1 US-10-418-182-215 Sequen 13 10.6 50.5 15 1 US-10-418-182-99 Sequen 14 10.4 49.5 12 1 US-09-947-209A-19 Sequen 15 10.4 49.5 12 1 US-09-947-209A-19 Sequen 17 10.4 49.5 12 1 US-10-099-379-19 Sequen 18 10.4 49.5 12 1 US-10-099-379-19 Sequen 19 10.4 49.5 12 1 US-10-099-379-19 Sequen 19 10.4 49.5 12 1 US-10-099-379-19 Sequen 20 10.4 49.5 12 1 US-10-092-379-19 Sequen 20 10.4 49.5 12 1 US-10-257-017B-31912 Sequen 20 10.4 49.5 12 1 US-10-257-017B-31912 Sequen 20 10.4 49.5 13 1 US-10-257-017B-3109 Sequen 20 10.4 49.5 13 1 US-10-257-017B-31099 Sequen 30 10.4 49.5 13 1 US-10-257-017B-31099 Sequen 31 1 US-10-257-017B-31099 Sequen 31 1 US-10-257-017B-31099 Sequen 31 1 US-10-257-017B-31099 Sequen 31 1 US-30-257-017B-31099 Sequen 31 1 US-30-257-017B-30-309 Sequen 31 1 US-30-309 Sequen 31 1 US-30-309 Sequen 31 1 US-30-309 Sequen 31 1 US-30-309		8	•	54.3	13	Н	10-257-017B	70446,
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12 10.6 50.5 15 1 US-10-411-182-215 Sequen 10.6 50.5 15 1 US-10-411-182-215 Sequen 10.4 49.5 12 1 US-09-947-2094-19 Sequen 15 10.4 49.5 12 1 US-09-947-2094-19 Sequen 17 10.4 49.5 12 1 US-10-099-379-19 Sequen 18 10.4 49.5 12 1 US-10-099-379-19 Sequen 19 10.4 49.5 12 1 US-10-099-379-19 Sequen 20 10.4 49.5 12 1 US-10-099-379-19 Sequen 21 10.4 49.5 12 1 US-10-257-107B-31910 Sequen 22 10.4 49.5 12 1 US-10-257-017B-31912 Sequen 22 10.4 49.5 12 1 US-10-257-017B-31912 Sequen 23 10.4 49.5 13 1 US-10-257-017B-31109 Sequen 24 10.4 49.5 13 1 US-10-257-017B-31049 Sequen 25 10.4 49.5 13 1 US-10-257-017B-3130297 Sequen 27 10.4 49.5 13 1 US-10-257-017B-3130297 Sequen 28 10.4 49.5 13 1 US-10-257-017B-3130297 Sequen 31 US-30-257-017B-3130297 Sequen 31 US-30-257-017B-330397 Sequen 31 US-30-2520049 Sequen 31 US-30-2530397 Sequen 31 US-30-2530397 SEQUEN 31 US-30-2530397 SEQUEN 31 US-30-25	υ	11	•	53.3	16	Н	US-10-043-875-402	402,
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ALIGNMENTS

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GenCore version 5.1.6
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Run on:

April 4, 2005, 14:51:31; Search time 0.001 Seconds (without alignments) 37.550 Million cell updates/sec

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Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 0.5

62 seqs, 751 residues

Searched:

124 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 66 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 73issdb:* Database :

SUMMARIES

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